

1647

RAW SEQUENCE LISTING DATE: 10/17/2000
 PATENT APPLICATION: US/09/285,531A TIME: 11:08:52

Input Set : A:\2891.1003-001 Substitute SEQ Listing.txt
 Output Set: N:\CRF3\10172000\I285531A.raw

Does Not Comply
 Corrected Diskette Needed

4 <110> APPLICANT: Chernajovsky, Yuti
 5 Neve, Richard
 6 Feldmann, Marc
 8 <120> TITLE OF INVENTION: Small Molecular Weight TNF Receptor Multimeric Molecule
 10 <130> FILE REFERENCE: KIR95-01A
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/285,531A
 C--> 12 <141> CURRENT FILING DATE: 1999-04-02
 12 <150> PRIOR APPLICATION NUMBER: 08/437,533
 13 <151> PRIOR FILING DATE: 1995-05-09
 15 <160> NUMBER OF SEQ ID NOS: 4
 17 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1506
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Artificial Sequence
 W--> 24 <220> FEATURE: Open Reading Frame of Human P75 TNF-R ECD
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (1)...(1506)
 W--> 28 <223> OTHER INFORMATION:
 28 <400> SEQUENCE: 1
 29 atg gcg ccc gtc gcc gtc tgg gcc gcg ctg gcc gtc gga ctg gag ctc 48
 30 Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
 31 1 5 10 15
 33 tgg gct gcg gcg cac gcc ttg ccc gcc cag gtg gca ttt aca ccc tac 96
 34 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
 35 20 25 30
 37 gcc ccg gag ccc ggg agc aca tgc cgg ctc aga gaa tac tat gac cag 144
 38 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
 39 35 40 45
 41 aca gct cag atg tgc tgc agc aaa tgc tgc ccg ggc caa cat gca aaa 192
 42 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
 43 50 55 60
 45 gtc ttc tgt acc aag acc tgc gac acc gtg tgt gac tcc tgt gag gac 240
 46 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
 47 65 70 75 80
 49 agc aca tac acc cag ctc tgg aac tgg gtt ccc gag tgc ttg agc tgt 288
 50 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
 51 85 90 95
 54 ggc tcc cgc tgt agc tct gac cag gtg gaa act caa gcc tgc act cgg 336
 55 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
 56 100 105 110
 60 gaa cag aac cgc atc tgc acc tgc agg ccc gcc tgg tac tgc gcg ctg 384
 61 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
 62 115 120 125
 64 agc aag cag gag ggg tgc cgg ctg tgc gcg ccg ctg cgc aag tgc cgc 432
 65 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
 66 130 135 140

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68	ccg ggc ttc ggc gtg gcc aga cca gga act gaa aca tca gac gtg gtg	480
69	Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val	
70	145 150 155 160	
72	tgc aag ccc tgt gcc ccg ggg acg ttc tcc aac acg act tca tcc acg	528
73	Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Thr	
74	165 170 175	
76	gat att tgc agg ccc cac cag atc tgt aac gtg gtg gcc atc cct ggg	576
77	Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly	
78	180 185 190	
80	aat gca agc atg gat gca gtc tgc acg tcc acg tcc ccc acc cgg agt	624
81	Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser	
82	195 200 205	
84	atg gcc cca ggg gca gta cac tta ccc cag cca gtg tcc aca cga tcc	672
85	Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser	
86	210 215 220	
88	caa cac acg cag cca act cca gaa ccc agc act gct cca agc acc tcc	720
89	Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser	
90	225 230 235 240	
92	ttc ctg ctc cca atg ggc ccc agc ccc cca gct aga ggt ggg ggc ggt	768
93	Phe Leu Leu Pro Met Gly Pro Ser Pro Ala Arg Gly Gly Gly Gly	
94	245 250 255	
96	tcg ggt ggc ggc ggc tcg ggc ggg ggt ggc tcg gat ccc gcc cag gtg	816
97	Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp Pro Ala Gln Val	
98	260 265 270	
100	gca ttt aca ccc tac gcc ccg gag ccc ggg agc aca tgc cgg ctc aga	864
101	Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg	
102	275 280 285	
104	gaa tac tat gac cag aca gct cag atg tgc tgc agc aaa tgc tcg ccg	912
105	Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro	
106	290 295 300	
108	ggc caa cat gca aaa gtc ttc tgt acc aag acc tcg gac acc gtg tgt	960
109	Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys	
110	305 310 315 320	
112	gac tcc tgt gag gac agc aca tac acc cag ctc tgg aac tgg gtt ccc	1008
113	Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro	
114	325 330 335	
116	gag tgc ttg agc tgt ggc tcc cgc tgt agc tct gac cag gtg gaa act	1056
117	Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr	
118	340 345 350	
120	caa gcc tgc act cgg gaa cag aac cgc atc tgc acc tgc agg ccc ggc	1104
121	Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly	
122	355 360 365	
124	tgg tac tgc gcg ctg agc aag cag gag ggg tgc cgg ctg tgc gcg ccg	1152
125	Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro	
126	370 375 380	
128	ctg cgc aag tgc cgc ccg ggc ttc ggc gtg gcc aga cca gga act gaa	1200
129	Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu	
130	385 390 395 400	
132	aca tca gac gtg gtg tgc aag ccc tgt gcc ccg ggg acg ttc tcc aac	1248

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Input Set : A:\2851.1003-001 Substitute SEQ Listing.txt

Output Set: N:\CRF3\10172000\I285531A.raw

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133 Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn
134                               405                               410                               415
136 acg act tca tcc acg gat att tgc agg ccc cac cag atc tgt aac gtg      1296
137 Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val
138                               420                               425                               430
140 gtg gcc atc cct ggg aat gca agc atg gat gca gtc tgc acg tcc acg      1344
141 Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr
142                               435                               440                               445
144 tcc ccc acc cgg agt atg gcc cca ggg gca gta cac tta ccc cag cca      1392
145 Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val His Leu Pro Gln Pro
146                               450                               455                               460
148 gtg tcc aca cga tcc caa cac acg cag cca act cca gaa ccc agc act      1440
149 Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr
150 465                               470                               475                               480
152 gct cca agc acc tcc ttc ctg ctc cca atg ggc ccc agc ccc cca gct      1488
153 Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala
154                               485                               490                               495
156 gaa ggg agc act ggc tag      1506
157 Glu Gly Ser Thr Gly *
158                               500
161 <210> SEQ ID NO: 2
162 <211> LENGTH: 501
163 <212> TYPE: PRT
164 <213> ORGANISM: Artificial Sequence
W--> 166 <220> FEATURE: Open Reading Frame of Human P75 TNF-R ECD
W--> 168 <223> OTHER INFORMATION:
168 <400> SEQUENCE: 2
169 Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
170 1 5 10 15
171 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
172 20 25 30
173 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
174 35 40 45
175 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
176 50 55 60
178 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
179 65 70 75 80
181 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
182 85 90 95
183 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
184 100 105 110
185 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
186 115 120 125
187 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
188 130 135 140
189 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
190 145 150 155 160
191 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
192 165 170 175

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```

193 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
194      180      185      190
195 Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
196      195      200      205
197 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
198      210      215      220
199 Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
200      225      230      235      240
201 Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Arg Gly Gly Gly Gly
202      245      250      255
203 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Pro Ala Gln Val
204      260      265      270
205 Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg
206      275      280      285
207 Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro
208      290      295      300
209 Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys
210      305      310      315      320
211 Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro
212      325      330      335
213 Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr
214      340      345      350
217 Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly
218      355      360      365
219 Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro
220      370      375      380
221 Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu
222      385      390      395      400
223 Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn
224      405      410      415
225 Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val
226      420      425      430
227 Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr
228      435      440      445
229 Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val His Leu Pro Gln Pro
230      450      455      460
231 Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr
232      465      470      475      480
233 Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala
234      485      490      495
235 Glu Gly Ser Thr Gly
236      500
238 <210> SEQ ID NO: 3
239 <211> LENGTH: 30
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: deoxyoligonucleotide primer
246 <400> SEQUENCE: 3

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247  tcggatcccg cccaggtggc atttacacc                      30
249 <210> SEQ ID NO: 4
250 <211> LENGTH: 20
251 <212> TYPE: DNA
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
255 <223> OTHER INFORMATION: deoxyoligonucleotide primer
257 <400> SEQUENCE: 4
258  cggaattcta gaaggtaccc                                      20
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VERIFICATION SUMMARY

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Input Set : A:\2891.1003-001 Substitute SEQ Listing.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:24 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:28 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:166 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:168 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: